

Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claim 1 (Original): A seed comprising at least one set of the chromosomes of maize inbred line PH94T, representative seed of said line having been deposited under ATCC Accession No. PTA-4692.

Claim 2 (Previously presented): A maize plant produced by growing the seed of claim 1.

Claim 3 (Original): A maize plant part of the maize plant of claim 2.

Claim 4 (Original): An F1 hybrid maize seed produced by crossing a plant of maize inbred line designated PH94T, representative seed of said line having been deposited under ATCC Accession No. PTA-4692, with a different maize plant and harvesting the resultant F1 hybrid maize seed, wherein said F1 hybrid maize seed comprises two sets of chromosomes and one set of the chromosomes is the same as maize inbred line PH94T.

Claim 5 (Original): A maize plant produced by growing the F1 hybrid maize seed of claim 4.

Claim 6 (Original): A maize plant part of the maize plant of claim 5.

Claim 7 (Currently amended): An F1 hybrid maize seed comprising an inbred ~~corn~~ maize plant cell of inbred maize line PH94T, representative seed of said line having been deposited under ATCC Accession No. PTA-4692.

Claim 8 (Original): A maize plant produced by growing the F1 hybrid maize seed of claim 7.

Claim 9 (Currently amended): The F1 hybrid maize seed of claim 7 wherein the inbred ~~corn~~ maize plant cell comprises two sets of chromosomes of maize inbred line PH94T.

Claim 10 (Original): A maize plant produced by growing the F1 hybrid maize seed of claim 9.

Claim 11 (Previously presented): The seed of claim 1, wherein said set of chromosomes comprise all of the alleles of inbred line PH94T at the SSR loci listed in Table 4.

Claim 12 (Previously presented): The F1 hybrid maize seed of claim 4 wherein the set of chromosomes that is the same as maize inbred line PH94T comprises all of the alleles of inbred line PH94T at the SSR loci listed in Table 4.

Claim 13 (Previously presented): A process of introducing a desired trait into maize inbred line PH94T comprising:

- (a) crossing PH94T plants grown from PH94T seed, representative seed of which has been deposited under ATCC Accession Number PTA-4692, with plants of another maize line that comprise a desired trait to produce F1 progeny plants, wherein the desired trait is selected from the group consisting of waxy starch, male sterility, herbicide resistance, insect resistance, bacterial disease resistance, fungal disease resistance, and viral disease resistance;
- (b) selecting F1 progeny plants that have the desired trait to produce selected F1 progeny plants;
- (c) crossing the selected progeny plants with the PH94T plants to produce backcross progeny plants;
- (d) selecting for backcross progeny plants that have the desired trait and the alleles of inbred line PH94T at the SSR loci listed in Table 4 to produce selected backcross progeny plants; and
- (e) repeating steps (c) and (d) to produce backcross progeny plants that comprise the desired trait and comprise at least 95% of the alleles of inbred line PH94T at the SSR loci listed in Table 4.

Claim 14 (Previously presented): A plant produced by the process of claim 13, wherein the plant comprises at least 95% of the alleles of inbred line PH94T at the SSR loci listed in Table 4.

Claim 15 (Previously presented): A maize plant having all the physiological and morphological characteristics of inbred line PH94T, wherein a sample of the seed of inbred line PH94T was deposited under ATCC Accession Number PTA-4692.

Claim 16 (Currently amended): A process of producing maize seed, comprising crossing a first parent maize plant with a second parent maize plant, wherein one or both of the first or the second parent maize plants is the plant of claim 15, ~~wherein seed is allowed to form and harvesting seed.~~

Claim 17 (Previously presented): The maize seed produced by the process of claim 16.

Claim 18 (Previously presented): The maize seed of claim 17, wherein the maize seed is hybrid seed.

Claim 19 (Previously presented): A hybrid maize plant, or its parts, produced by growing said hybrid seed of claim 18.

Claim 20 (Previously presented): A maize seed produced by growing said maize plant of claim 19 and harvesting the resultant maize seed.

Claim 21 (Previously presented): The maize plant of claim 15, further comprising an SSR profile in accordance with the profile shown in Table 4.

Claim 22 (Previously presented): A cell of the maize plant of claim 15.

Claim 23 (Previously presented): The cell of claim 22, wherein said cell is further defined as having an SSR profile in accordance with the profile shown in Table 4.

Claim 24 (Previously presented): A seed comprising the cell of claim 22.

Claim 25 (Currently amended): The maize plant of claim 15, further defined as having a genome comprising a single locus gene conversion.

Claim 26 (Currently amended): The maize plant of claim 25, wherein the single locus gene was stably inserted into a maize genome by transformation.

Claim 27 (Currently amended): The maize plant of claim 25, wherein the locus gene is selected from the group consisting of a dominant allele and a recessive allele.

Claim 28 (Currently amended): The maize plant of claim 25, wherein the locus gene confers a trait selected from the group consisting of herbicide tolerance; insect resistance; resistance to bacterial, fungal, nematode or viral disease; yield enhancement; waxy starch; improved nutritional quality; male sterility and restoration of male fertility.

Claim 29 (Previously presented): The maize plant of claim 15, wherein said plant is further defined as comprising a gene conferring male sterility.

Claim 30 (Previously presented): The maize plant of claim 15, wherein said plant is further defined as comprising a transgene conferring a trait selected from the group consisting of male sterility, herbicide resistance, insect resistance and disease resistance.

Claim 31 (Previously presented): A method of producing a maize plant derived from the inbred line PH94T, the method comprising the steps of:

- (a) growing a progeny plant produced by crossing the plant of claim 15 with a second maize plant;
- (b) crossing the progeny plant with itself or a different plant to produce a seed of a progeny plant of a subsequent generation;
- (c) growing a progeny plant of a subsequent generation from said seed and crossing the progeny plant of a subsequent generation with itself or a different plant; and

- (d) repeating steps (b) and (c) for an additional 0-5 generations to produce a maize plant derived from the inbred line PH94T.

Claim 32 (Previously presented): The method of claim 31 wherein the maize plant derived from the inbred line PH94T is an inbred maize plant.

Claim 33 (Previously presented): The method of claim 32, further comprising the step of crossing the inbred maize plant derived from the inbred line PH94T with a second, distinct inbred maize plant to produce an F1 hybrid maize plant.

Claim 34 (Previously presented): A method for developing a maize plant in a maize plant breeding program using plant breeding techniques comprising employing a maize plant, or its parts, as a source of plant breeding material comprising using the maize plant of claim 15, or parts thereof, as a source of said breeding material.

Claim 35 (Previously presented): The method for developing a maize plant in a maize plant breeding program of claim 34 wherein plant breeding techniques are selected from the group consisting of recurrent selection, backcrossing, pedigree breeding, restriction fragment length polymorphism enhanced selection, genetic marker enhanced selection, and transformation.

Claim 36 (Previously presented): The method of claim 35 wherein the plant breeding technique comprises the steps of:

- (a) obtaining the molecular marker profile of maize inbred line PH94T;
- (b) obtaining an F1 hybrid seed for which maize inbred line PH94T is a parent;
- (c) inducing doubled haploidy of the F1 hybrid seed to create progeny without the occurrence of meiotic segregation; and
- (d) selecting progeny that retain the molecular marker profile of PH94T.